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P#53 1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/325,278B

DATE: 10/10/2002
TIME: 10:34:28

Input Set : D:\402.app.txt
Output Set: N:\CRF4\10102002\H325278B.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

C--> 6 (i) APPLICANT: Bjorck, Lars
7 Sjobring, Ulf
9 (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
11 (iii) NUMBER OF SEQUENCES: 15
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Seed IP Law Group
15 (B) STREET: 701 Fifth Avenue Suite 6300
16 (C) CITY: Seattle
17 (D) STATE: Washington
18 (E) COUNTRY: USA
19 (F) ZIP: 98104-7092
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US/08/325,278B
C--> 29 (B) FILING DATE: 26-Oct-1994
30 (C) CLASSIFICATION:
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Potter, Jane E. R.
34 (B) REGISTRATION NUMBER: 33,332
35 (C) REFERENCE/DOCKET NUMBER: 100084.402
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (206) 622-4900
39 (B) TELEFAX: (206) 682-6031
42 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 305 amino acids
46 (B) TYPE: amino acid
47 (C) STRANDEDNESS: unknown
48 (D) TOPOLOGY: unknown
50 (ii) MOLECULE TYPE: protein
52 (iii) HYPOTHETICAL: NO
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
62 1 5 10 15
64 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser

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65 20 25 30
 67 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
 68 35 40 45
 70 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
 71 50 55 60
 73 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 74 65 70 75 80
 76 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 77 85 90 95
 79 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 80 100 105 110
 82 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 83 115 120 125
 85 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 86 130 135 140
 88 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 89 145 150 155 160
 91 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 92 165 170 175
 94 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
 95 180 185 190
 97 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 98 195 200 205
 100 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 101 210 215 220
 103 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 104 225 230 235 240
 106 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 107 245 250 255
 109 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 110 260 265 270
 112 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 113 275 280 285
 115 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 116 290 295 300
 118 Glu
 119 305
 121 (2) INFORMATION FOR SEQ ID NO: 2:
 123 (i) SEQUENCE CHARACTERISTICS:
 124 (A) LENGTH: 921 base pairs
 125 (B) TYPE: nucleic acid
 126 (C) STRANDEDNESS: double
 127 (D) TOPOLOGY: unknown
 129 (ii) MOLECULE TYPE: DNA (genomic)
 131 (iii) HYPOTHETICAL: NO
 133 (vi) ORIGINAL SOURCE:
 134 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
 138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 140 GCGGTAGAAA ATAAAGAAGA AACACCAGAAA ACACCAGAAA CTGATTCAAGA AGAAGAAGTA

140 GCGGTAGAAA ATAAAGAAGA AACACCCAGAA ACACCCAGAAA CTGATTCAAGA AGAAGAAGTA

60

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142	ACAATCAAAG	CTAACCTAAT	CTTTGCAAAT	GGAAGCACAC	AAACTGCAGA	ATTCAAAGGA	120
144	ACATTTGAAA	AAGCAACATC	AGAAGCTTAT	GCGTATGCAG	ATACTTGTAA	GAAAGACAAT	180
146	GGAGAATATA	CTGTAGATGT	TGCAGATAAA	GGTTATACTT	TAAATATTAA	ATTGCTGGA	240
148	AAAGAAAAAA	CACCAAGAAGA	ACCAAAAGAA	GAAGTTACTA	TTAAAGCAAA	CTTAATCTAT	300
150	GCAGATGGAA	AAACACAAAC	AGCAGAATTC	AAAGGAACAT	TTGAAGAACG	AACAGCAGAA	360
152	GCATACAGAT	ATGCAGATGC	ATTAAGAAG	GACAATGGAG	AATATACAGT	AGACGTTGCA	420
154	GATAAAGGTT	ATACTTTAAA	TATTAATTG	GCTGGAAAAG	AAAAAACACC	AGAAGAACCA	480
156	AAAGAAGAAG	TTACTATTAA	AGCAAACTTA	ATCTATGCAG	ATGGAAAAAC	ACAAACAGCA	540
158	GAATTCAAAG	GAACATTTGA	AGAAGCAACA	GCAGAAGCAT	ACAGATATGC	TGACTTATTA	600
160	GCAAAAGAAA	ATGGTAAATA	TACAGTAGAC	GTTGCAGATA	AAGGTTATAC	TTTAAATATT	660
162	AAATTGCTG	AAAAAGAAAA	AACACCAGAA	GAACCAAAAG	AAGAAGTTAC	TATTAAGCA	720
164	AACTTAATCT	ATGCAGATGG	AAAAACTCAA	ACAGCAGAGT	TCAAAGGAAC	ATTGCGAGAA	780
166	GCAACAGCAG	AAGCATACAG	ATACGCTGAC	TTATTAGCAA	AAGAAAATGG	TAATATACA	840
168	GCAGACTTAG	AAGATGGTGG	ATACACTATT	AATATTAGAT	TTGCAGGTAA	GAAAGTTGAC	900
170	AAAAAACAG	AAGAATAATA	A				921

172 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 434 amino acids
176 (B) TYPE: amino acid
177 (C) STRANDEDNESS: unknown
178 (D) TOPOLOGY: unknown

180 (ii) MOLECULE TYPE: protein

182 (iii) HYPOTHETICAL: NO

184 (vi) ORIGINAL SOURCE:

185 (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

191	Ala	Val	Glu	Asn	Lys	Glu	Glu	Thr	Pro	Glu	Thr	Pro	Glu	Thr	Asp	Ser
192	1					5				10					15	
194	Glu	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Phe	Ala	Asn	Gly	Ser
195						20				25				30		
197	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Lys	Ala	Thr	Ser	Glu
198						35			40			45				
200	Ala	Tyr	Ala	Tyr	Ala	Asp	Thr	Leu	Lys	Lys	Asp	Asn	Gly	Glu	Tyr	Thr
201						50			55			60				
203	Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly
204						65			70			75			80	
206	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala
207						85			90			95				
209	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly
210						100			105			110				
212	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu	Ala	Tyr	Arg	Tyr	Ala	Asp	Ala	Leu
213						115			120			125				
215	Lys	Lys	Asp	Asn	Gly	Glu	Tyr	Thr	Val	Asp	Val	Ala	Asp	Lys	Gly	Tyr
216						130			135			140				
218	Thr	Leu	Asn	Ile	Lys	Phe	Ala	Gly	Lys	Glu	Lys	Thr	Pro	Glu	Glu	Pro
219						145			150			155			160	
221	Lys	Glu	Glu	Val	Thr	Ile	Lys	Ala	Asn	Leu	Ile	Tyr	Ala	Asp	Gly	Lys
222						165			170			175				
224	Thr	Gln	Thr	Ala	Glu	Phe	Lys	Gly	Thr	Phe	Glu	Glu	Ala	Thr	Ala	Glu

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225 180 185 190
227 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
228 195 200 205
230 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
231 210 215 220
233 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
234 225 230 235 240
236 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
237 245 250 255
239 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
240 260 265 270
242 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
243 275 280 285
245 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
246 290 295 300
248 Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
249 305 310 315 320
251 Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
252 325 330 335
254 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
255 340 345 350
257 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
258 355 360 365
260 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
261 370 375 380
263 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
264 385 390 395 400
266 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
267 405 410 415
269 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
270 420 425 430
272 Glu Met

275 (2) INFORMATION FOR SEQ ID NO: 4:

277 (i) SEQUENCE CHARACTERISTICS:
278 (A) LENGTH: 1308 base pairs
279 (B) TYPE: nucleic acid
280 (C) STRANDEDNESS: double
281 (D) TOPOLOGY: unknown
283 (ii) MOLECULE TYPE: DNA (genomic)
285 (iii) HYPOTHETICAL: NO
287 (vi) ORIGINAL SOURCE:
288 (A) ORGANISM: Escherichia coli L392/pHDLG, DSM 7055
292 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

294 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA	60
295 CTGATTTCAGA AGAAGAAGTA	
296 ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC	120
297 AAACTGCAGA ATTCAAAGGA	
298 ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTGAA GAAAGACAAT	180
300 GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTGCTGGA	240
302 AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT	300
304 GCAGATGGAA AAACACAAAC AGCAGAATTG AAAGGAACAT TTGAAGAAC AACAGCAGAA	360

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306	GCATACAGAT	ATGCAGATGC	ATTAAGAAG	GACAATGGAG	AATATACAGT	AGACGTTGCA	420
308	GATAAAGGTT	ATACTTTAAA	TATTAATTG	GCTGGAAAAG	AAAAAACACC	AGAAGAACCA	480
310	AAAGAAGAAG	TTACTATTAA	AGCAAACCTTA	ATCTATGCAG	ATGGAAAAAC	ACAAACAGCA	540
312	GAATTCAAAG	GAACATTGAA	AGAACCAACA	GCAGAAGCAT	ACAGATATGC	TGACTTATTAA	600
314	GCAAAAGAAA	ATGGTAAATA	TACAGTAGAC	GTTGCAGATA	AAGGTTTAC	TTTAAATATT	660
316	AAATTGCTG	GAAAAGAAAA	AACACCAGAA	GAACCAAAAG	AAGAAGTTAC	TATTAAGCA	720
318	AACTTAATCT	ATGCAGATGG	AAAAACTCAA	ACAGCAGAGT	TCAAAGGAAC	ATTGAGCAGAA	780
320	GCAACAGCAG	AAGCATACAG	ATACGCTGAC	TTATTAGCAA	AAGAAAATGG	TAAATATACA	840
322	GCAGACTTAG	AAGATGGTGG	ATACACTATT	AATATTAGAT	TGCGAGGTAA	GAAAGTTGAC	900
324	GAAAACCAG	AAGAACCCAT	GGACACTTAC	AAATTAATCC	TTAATGGTAA	AACATTGAAA	960
326	GGCGAAACAA	CTACTGAAGC	TGTTGATGCT	GCTACTGCAG	AAAAAGTCTT	CAAACAATAC	1020
328	GCTAACGACA	ACGGTGTGAA	CGGTGAATGG	ACTTACGACG	ATGCGACTAA	GACCTTTACA	1080
330	GTTACTGAAA	AACCAGAAAGT	GATCGATGCC	TCTGAATTAA	CACCAGCCGT	GACAACCTTAC	1140
332	AAACTTGTAA	TTAATGGTAA	AACATTGAAA	GGCGAAACAA	CTACTAAAGC	AGTAGACGCA	1200
334	GAAACTGCAG	AAAAAGCCTT	CAAACAATAC	GCTAACGACA	ACGGTGTGAA	TGGTGTGTTGG	1260
336	ACTTATGATG	ATGCAGACTAA	GACCTTTACG	GTAACGTAAA	TGTAATAAA		1308

338 (2) INFORMATION FOR SEQ ID NO: 5:

340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 1332 base pairs
342 (B) TYPE: nucleic acid
343 (C) STRANDEDNESS: double
344 (D) TOPOLOGY: unknown
346 (ii) MOLECULE TYPE: DNA (genomic)
348 (iii) HYPOTHETICAL: NO
351 (ix) FEATURE:

352 (A) NAME/KEY: CDS
353 (B) LOCATION: 1..1329

356 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

358	AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC	48
359	Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn	
360	1 5 10 15	
362	AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA	96
363	Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu	
364	20 25 30	
366	AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG	144
367	Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys	
368	35 40 45	
370	AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT	192
371	Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg	
372	50 55 60	
374	AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA	240
375	Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu	
376	65 70 75 80	
378	GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA	288
379	Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu	
380	85 90 95	
382	GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG	336
383	Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg	
384	100 105 110	

VERIFICATION SUMMARY
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L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]